Amendments to the Claims:

The following listing of claims replaces all prior versions and listings of the claims in this application.

Listing of the Claims:

Original 1-18. (Cancelled)

19-42. presented during International Processing. (Cancelled)

43. (New) A method of screening a test nucleic acid sequence to identify a candidate nucleic acid sequence encoding an antimicrobial peptide, said method comprising:

(a) identifying an initial peptide of interest;

(b) identifying a DNA sequence from a first fish species containing a nucleotide sequence encoding the initial peptide;

(c) identifying within the DNA sequence a flanking nucleotide sequence on each side of the peptide-encoding sequence;

(d) obtaining a primer oligonucleotide sequence complementary to each flanking sequence; and

(e) screening a test nucleic acid sequence from a fish species other than the first fish species to determine whether it is capable of being amplified by PCR using the primers from step (d); amplification indicating that the test nucleic acid sequence is a candidate nucleic acid sequence encoding an antimicrobial peptide.

44. (New) The method of claim 43 wherein the initial peptide has a net positive charge of at least 2 and has an amphipathic structure.

45. (New) The method of claim 43 wherein the initial peptide is selected from the group consisting of a hepcidin, a pleurocidin, a pardaxin, a misgurin, HFA-1, a piscidin, a moronecidin, and a cleavage product of histone 2A from catfish.

46. (New) The method of claim 45 wherein the cleavage product of histone 2A is a parasin.

47. (New) The method of claim 43 comprising a further step (f) of predicting the amino acid sequence encoded by the candidate sequence and selecting nucleic acid sequences which are predicted to encode peptides having an amphipathic structure and a net charge.

48. (New) The method of claim 47 comprising a further additional step of obtaining a peptide corresponding to the candidate nucleic acid sequence and assaying the peptide sequence for antimicrobial activity.

49. (New) The method of claim 43 comprising a further step (a') of confirming that the initial peptide has antimicrobial activity.

50. (New) The method of claim 43 wherein the initial peptide is a pleurocidin.

51. (New) The method of claim 50 wherein at least one of the flanking sequences is selected from the group consisting of a nucleotide sequence encoding signal sequence I (SEQ ID NO: 305), a nucleotide sequence encoding Acidic Sequence I (SEQ ID NO: 306), GCCCACTTTGTATTCGCAAG (SEQ ID NO: 5) and CTGAAGGCTCCTTCAAGGCG (SEQ ID NO: 6).

52. (New) The method of claim 43 wherein the initial peptide is a hepcidin.

53. (New) The method of claim 52 wherein at least one flanking sequence is selected from the group consisting of a nucleotide sequence encoding signal peptide II (SEQ ID NO: 307), a nucleotide sequence encoding signal peptide III (SEQ ID NO: 308), a nucleotide sequence encoding signal peptide IV (SEQ ID NO: 309), a nucleotide sequence encoding signal peptide V (SEQ ID NO: 310), a nucleotide sequence encoding prosequence I (SEQ ID NO: 311), a nucleotide sequence encoding prosequence II (SEQ ID NO: 312), ACAACCTCGTCCTTAGG (SEQ ID NO: 313) and ACGCCCGTCCAGGAAT (SEQ ID NO: 314).

54. (New) An isolated nucleic acid sequence identifiable using the method of claim 43.

55. (New) The nucleic acid sequence of claim 54 wherein the sequence is selected from the group consisting of SEQ ID NOS: 82-124, 129-173 and 327.

56. (New) An isolated polypeptide capable of being encoded by the nucleic acid sequence of claim 54.

57. (New) A kit comprising:

a. a first nucleic acid sequence at least 95 % identical to a first flanking sequence, located at or near a 5' end of a target sequence encoding an antimicrobial peptide;

b. a second nucleic acid sequence at least 95 % identical to a second flanking sequence located at or near a 3' end of a target sequence encoding an antimicrobial peptide; and

c. instructions for carrying out the method of claim 43.

58. (New) The method of claim 43, wherein at least one sequence selected from the group consisting of signal sequence I, acidic sequence I, signal peptide II, signal peptide III, signal peptide IV, signal peptide V, prosequence I, prosequence II, nucleic acid sequences encoding them, and nucleic acid sequences substantially complementary to such encoding nucleic acids, is identified.

59. (New) An isolated antimicrobial peptide at least 80% homologous to one of peptide a, b, c or d:

Peptide a	GW(G/K)XXFXK
Peptide b	GXXXXXXXHXGXXIH
Peptide c	FKCKFCCGCCXXGVCGXCC
Peptide d	CXXCCNCC(K/H)XKGCGFCCKF
Peptide e	FKCKFCCGCRCGXXCGLCCKF
Peptide f	XXXCXXCCNXXGCGXCCKX

60. (New) The antimicrobial peptide of claim 59 which is at least 90% homologous to one of peptide a, b, c or d.

61. (New) The antimicrobial peptide of claim 59 which is one of peptide a, b, c or d.

62. (New) A method of screening a test nucleic acid sequence to identify a candidate nucleic acid sequence encoding an antimicrobial peptide, said peptide comprising:

a) identifying a nucleic acid sequence encoding an initial peptide of interest;

(b) identifying a DNA sequence from a first fish species containing a nucleotide sequence encoding the initial peptide;

(c) identifying within the DNA sequence a flanking nucleotide sequence on each side of the peptide-encoding sequence;

(d) obtaining a primer oligonucleotide sequence complementary to each flanking sequence; and

(e) screening a test nucleic acid sequence from a fish species other that the first fish species to determine whether it is capable of being amplified by PCR using the primers from step (d); amplification indicating that the test nucleic acid sequence is a candidate nucleic acid sequence encoding an antimicrobial peptide.

63. (New) An isolated antimicrobial peptide selected from the group consisting of:

(a) WLRRIGKGVKIIGGAALDHL;

(b) GRRKRKWLRRIGKGVKIIGGAALDHL;

(c) RWGKWFKKATHVGKHVGKAALTAYL;

(d) RSTEDIIKSISGGGFLNAMNA;

(e) FFRLLFHGVHHGGGYLNAA;

(f) FFRLLFHGVHHVGKIKPRA;

(g) GWKSVFRKAKKVGKTVGGLALDHYL;

(h) GWKKWFNRAKKVGKTVGGLAVDHYL;

(i) GWRTLLKKAEVKTVGKLALKHYL;

(j) AGWGSIFKHIFKAGKFIHGAIQAHND;

(k) GFWGKLFKLGLHGIGLLHLHL;

(l) GWKKWLRKGAKHLGQAAIK;

(m) GWKKWLRKGAKHLGQAAIKGLAS;

(n) GWKKWFTKGERLSQRHFA;

(o) FLGLLFHGVHHVGKWIHGLIHGHH;

(p) GFLGILFHGVHHGRKKALHMNSERRS;

(q) FLGFLFHGIHHGIRAIHLIHG;

(r) FFGALIKGAIHGGKLLHKLIKKKHEHHGYGKHWG;

(s) FLGFLFHGIRHGIKAIHGMIHG;

(t) GKGRWLERIGKAGGIIIGGALDHLG;

(u) GLGNWMGPHISGEKKALHMNSERRS;

(v) GLGNWIVRPIGGEKKALQMNSERRS;

(w) LFGKFLKKVVHAGTSIGETALHVAAEHHGLHAHHG;

(x) GLGNWMGPHISGRKKALHMNSERRS;

(y) FLGLLFHGVHHVGKLIHGLIHG;

(z) ARWGTFFKHIFKAGRFIHGAIQAHNDG;

(aa) AWIPALNRIYHGALLRINRQMVYYRRHWHG;

(ab) AWMPALNRIYHGALLRINRQMVYYRRHWHG;

(ac) GWKKWFTKGAKHLGQAAINGLAS;

(ad) GWKKWLRKGAKHLGQAAIKGLAS;

(ae) FGDFYMKPGRKISHGYIRSPYG;

(af) GYWRFRNHRGERLSQRHFA;

(ag) FGMLFHRVHHAGRLIHRFIKRHG;

(ah) IFGLIATAVHNAGRLIHRLLGFHHGPPGFWHG;

(ai) IFGLIATAVHNVGRLVHGLLGFHHGPPGFWHG;

(aj) IFGLIATAVHNVGRLVHGLLGFHHGPPRFWHG;

(ak) FFGMRFHGVHHAGGGFLNAQGLLPSLLLNPGYRG;

(al) FFGALLKGAQALHGIIHNARHG;

(am) GWKDWFRKAKKVGKTVGGLALNHYLG;

(an) GIRKWFKKAAHVGKEVGKVALNACL;

(ao) GLKKWFKKAVHVGKKVGKVALNAYLG;

(ap) GWRKWIKKATHVGKHIGKAALDAYIG;

(aq) GCKKWFKKAAHVGKNVGKVALNAYLG;

(ar) GIRKWFKKAAHVGKKVGKVALNAYLG;

(as) WLERKWFKKATHVGKHVGKAALDAYLG;

(at) FFGLLFHGIHHAGKLIHGLIHHG;

(au) LGNWMGPHISGRKKALQMNSERRS;

(av) FLGLLFHGVHHVGNLIHGLIHHG;

(aw) GIRKWFKKAAHVGKKVGKVALNAYLG;

(ax) a C-terminally amidated or otherwise C-terminally or N- terminally modified peptide of (a) to (z) or (aa) to (aw);

(ay) a C-terminally amidated peptide of (a) to (z) or (aa) to (aw) where modification replaces C-terminal G; and

(az) a peptide of (a) to (z) or (aa) to (aw) comprising at least one conservative amino acid substitution or deletion of an amino acid residue thereof.

64. (New) An isolated nucleotide sequence encoding a peptide of claim 63.

65. (New) An isolated antimicrobial peptide selected from the group consisting of:

(a) MKTFSVAVAVVVVLACMFILESTAVPFSEVRTEEVESIDSPVGEHQQ-PGGTSMNLPMHFRFKRQSHLSLCRWCCNCCHNKGCGFCCKF;

(b) MKTFSVAVAVVVVLACMFILESTAVPFSEVRTEEVESIDSPVGEHQ-QPGGTSMNLPMHFRFKRQSHLSLCRWCCNCCHNKGCGFCCKF;

(c) MKAFSVAVVLVIACMFILESTAVPFSEVRTEEVGSFDSPVGEHQQP-GGESMHLPEPFRFKRQIHLSLCGLCCNCCHNIGCGFCCKF;

(d) RTEEVESIDSPVGEHQQPGGTSMNLPMHFRFKRQSHLSLCRWCC-NCCHNKGCGFCCKF;

(e) MKTFSVAVVPVIACMFILESTAVPFSEVRTEEVGSFDSPVGEHQQP-GGTSMNLPMHFRFKRQSHLSLCRWCFNCCHNKGCGFCCKF;

(f) MKQFSVAVVLVMACMFIVESTAVPFSEVRTEEVGSLDSPVGEHQQ-PGGESMHLPEPFRFKRQIHLSLCGLCCNCCHNIGCGFCCKF;

(g) MKAFSIAVAVTLVLAFVCIQCSSAVPFQGVQELEEAGGNDTPVAEH-QVMSMESWMENPTRQKRHISHISLCRWCCNCCKANKGCGFCCKF;

(h) MKTFSVAVAVTLVLAFVCIQDSSAVPFQGVQELEEAGGNDTPVAAH-QMMSMESWMESPVRQKRHISHISMCRWCCNCCKAKGCGPCCKF;

(i) MKTFSVAVTVAVVLVFICIQQSSGTFPEVQELEEAVSNDNAAAEHQ-ETSVDSWMMPYNRQKRAFKCKFCCGCCRAGVCGLCCKF;

(j) MKTFSVAVTVAVVLVFICIQQSSASFPEAQELEEAVSNDNAAAEHQ-ETPVDSWMMPYNRQKRSFKCKFCCGCCRAGVCGLCCKF;

(k) MKTFSVAVTVAVVLVFICIQQSSASFPEAQELEEAVSNDNAAAEHQ-ETPVDSWMMPNNRQKRGFKCKFCCGCCRAGVCGLCCKF;

(l) MKTFSVAVTVAVVLVFICIQQSSATFPEMPYNRQKRGFKCKFCCG-CCGAGVCGMCCKF;

(m) MKTFSVAVTVAVVLVFICIQQSSASFPEAQELEEAVSNDNAAAEHQ-ETPVDSRIPYNRQKRSFKCKFCCGCCRAGVCGLCCKF;

(n) MKTCSVAVTVAVVLVFICIQQSSASFPEVQELEEAVSNDNAAAEHQ-ETPVDSWMMPNNRQKRGFKCKFCCGCCRAGVCGLCCKF;

(o) MKTISVAVTVAVVLVFICIQQSSASFPEAQELEEAVSNDNAAAEHQE-TPVDSGMIPYNRQKRSFKCKFCCGCCRAGVCGLCCKF;

(p) MKTFSGAVTVAVVLVFICIQQSSASFPEVQELEEAVSNDNAAAEHQ-ETPVDSWMMPNNRQKRGFKCKFCCGCCRAGVCGLCCKF;

(q) MKTSVVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAAHQ-ETSVDSWMMPYNRPKRSFKCKFCCGCCRA-GVCGLCCKF;

(r) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETSVDSWMMPYNRPKRSFKCKFCCGCCRAGVCGLCCKF;

(s) MKTFVVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETSVDSWMMPYNRQKRSFKCKFCCGCCRAGVCGLCCKF;

(t) MKTSVVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAAHQ-ETSVDSWMMPYNRQKRSFKCKFCCGCCRAGVCGLCCKF;

(u) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETSVDLWMMPYNRQKRGFKCKFCCGCCSPGVCGLCCRF;

(v) MKTFSVAVAVAVVLIFICIQQSSATFPEVQELEEAVSNDNAAAEHQE-TSLDSWMMPYNRQKRGFKCKFCCGCCRAGVCGLCCKF;

(w) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETSLDSWMMPYNRHKRSFKCKFCCGCCRAGVCGLCCKF;

(x) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELGEAVSNDNAAAEHQ-ETSVDSWMMPYNRPKRSFKCKFCCGCCRAGVCGLCCKF;

(y) MKTFSVAVTVAVVLIFICIQQSSATSPEVQGLEEAVSNDNAAAEHQ-ETSVDSWMMPYNRQKRGFKCKFCCGCCRPGVCGLCCRS;

(z) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETSVDLWMMPYNRQKRGFKCKFCCGCCRPGVCGLCCRF;

(aa) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEH-QETSVDL-WMMPYNRQKRGFKCKFCCGCCSPGVCGLCCRF;

(ab) KTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQET-SVDS-WMMPYNRQKRGFKCKFCCGCCSPGVCGLCCKF;

(ac) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEH-QETSVDS-WMMPYNRQKRGFKCKFCCGCCRPGVCGLCCKF;

(ad) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETSVDSWMMPYNRQKRGFKCKFCCGCCRPGVCGLCCKF;

(ae) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETSVDSWMMPYNRQKRGFKCKFCCGCCRPGVCGLCCRF;

(af) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSSDNAAAEHQ-ETSVDSWMMPYNRQKRSFKCKFCCGCCRRGVCGLCCKF;

(ag) MKTISVAVTVAVVLLFICTQQSSATFPEVQELEEAVSSDNAAAEHQ-ETSVDSWMMPYNRQKRGFKCKFCCGCRCGALCGLCCKF;

(ah) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEPVSSDNAAAEH-QETSVDSWMMPYNRQKRGFKCKFCCGCRCGALCGLCCKF;

(ai) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSSDNAAAEHQ-ETSVDSWMMPYNRQKRGFKCKFCCGCRCGALCGLCCKF;

(aj) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETPVDSGMMPNNRQKRSADCWPCCNQNGCGTCCKV;

(ak) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEH-QETSVDSWMMPYNRQKRSAECSFCCNESGCGICCKF;

(al) MKTFSVAVTVAVVLVFICIQQSSATFPEVQELEEAVSNDNAAAEHQ-ETSVDSWMMPYNRQKRSAECSFCCNESGCGICCKF;

(am)MPNNRQKRGSNCKPCCNHNGCGTCCEV;

(an) a C-terminally amidated peptide (a) to (z) or (aa) to (am); and

(ao) a peptide of (a) to (z) or (aa) to (am) comprising at least one conservative amino acid substitution of an amino acid residue thereof.

66. (New) An isolated nucleotide sequence encoding a peptide of claim 65.